



SEQUENCE LISTING

<110> Heartlein, Michael W.
Lemontt, Jeffrey F.
Concino, Michael F.

B
<120> CHIMERIC PROTEINS FOR USE IN TRANSPORT
OF A SELECTED SUBSTANCE INTO CELLS

<130> 10278-025004

<140> US 09/753,385

<141> 2001-01-03

<150> US 08/470,058

<151> 1995-06-06

<150> US 09/037,188

<151> 1998-03-09

<150> US 09/285,310

<151> 1999-04-02

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3428

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14)...(3235)

<400> 1

agaggctgcg	agc	atg	ggg	ccc	tgg	ggc	tgg	aaa	ttg	cgc	tgg	acc	gtc	49
	Met	Gly	Pro	Trp	Gly	Trp	Lys	Leu	Arg	Trp	Thr	Val		
	1				5					10				

gcc	ttg	ctc	ctc	gcc	gcg	gcg	ggg	act	gca	gtg	ggc	gac	aga	tgt	gaa	97
Ala	Leu	Leu	Leu	Ala	Ala	Ala	Gly	Thr	Ala	Val	Gly	Asp	Arg	Cys	Glu	
	15						20					25				

aga	aac	gag	ttc	cag	tgc	caa	gac	ggg	aaa	tgc	atc	tcc	tac	aag	tgg	145
Arg	Asn	Glu	Phe	Gln	Cys	Gln	Asp	Gly	Lys	Cys	Ile	Ser	Tyr	Lys	Trp	
	30					35					40					

gtc	tgc	gat	ggc	agc	gct	gag	tgc	cag	gat	ggc	tct	gat	gag	tcc	cag	193
Val	Cys	Asp	Gly	Ser	Ala	Glu	Cys	Gln	Asp	Gly	Ser	Asp	Glu	Ser	Gln	
	45					50				55					60	

gag	acg	tgc	ttg	tct	gtc	acc	tgc	aaa	tcc	ggg	gac	ttc	agc	tgt	ggg	241
Glu	Thr	Cys	Leu	Ser	Val	Thr	Cys	Lys	Ser	Gly	Asp	Phe	Ser	Cys	Gly	

	65	70	75	
ggc cgt gtc aac cgc tgc att cct cag ttc tgg agg tgc gat ggc caa				289
Gly Arg Val Asn Arg Cys Ile Pro Gln Phe Trp Arg Cys Asp Gly Gln				
	80	85	90	
gtg gac tgc gac aac ggc tca gac gag caa ggc tgt ccc ccc aag acg				337
Val Asp Cys Asp Asn Gly Ser Asp Glu Gln Gly Cys Pro Pro Lys Thr				
	95	100	105	
tgc tcc cag gac gag ttt cgc tgc cac gat ggg aag tgc atc tct cgg				385
Cys Ser Gln Asp Glu Phe Arg Cys His Asp Gly Lys Cys Ile Ser Arg				
	110	115	120	
cag ttc gtc tgt gac tca gac cgg gac tgc ttg gac ggc tca gac gag				433
Gln Phe Val Cys Asp Ser Asp Arg Asp Cys Leu Asp Gly Ser Asp Glu				
	125	130	135	140
gcc tcc tgc ccg gtg ctc acc tgt ggt ccc gcc agc ttc cag tgc aac				481
Ala Ser Cys Pro Val Leu Thr Cys Gly Pro Ala Ser Phe Gln Cys Asn				
	145	150	155	
agc tcc acc tgc atc ccc cag ctg tgg gcc tgc gac aac gac ccc gac				529
Ser Ser Thr Cys Ile Pro Gln Leu Trp Ala Cys Asp Asn Asp Pro Asp				
	160	165	170	
tgc gaa gat ggc tgc gat gag tgg ccg cag cgc tgt agg ggt ctt tac				577
Cys Glu Asp Gly Ser Asp Glu Trp Pro Gln Arg Cys Arg Gly Leu Tyr				
	175	180	185	
gtg ttc caa ggg gac agt agc ccc tgc tgc gcc ttc gag ttc cac tgc				625
Val Phe Gln Gly Asp Ser Ser Pro Cys Ser Ala Phe Glu Phe His Cys				
	190	195	200	
cta agt ggc gag tgc atc cac tcc agc tgg cgc tgt gat ggt ggc ccc				673
Leu Ser Gly Glu Cys Ile His Ser Ser Trp Arg Cys Asp Gly Gly Pro				
	205	210	215	220
gac tgc aag gac aaa tct gac gag gaa aac tgc gct gtg gcc acc tgt				721
Asp Cys Lys Asp Lys Ser Asp Glu Glu Asn Cys Ala Val Ala Thr Cys				
	225	230	235	
cgc cct gac gaa ttc cag tgc tct gat gga aac tgc atc cat ggc agc				769
Arg Pro Asp Glu Phe Gln Cys Ser Asp Gly Asn Cys Ile His Gly Ser				
	240	245	250	
cgg cag tgt gac cgg gaa tat gac tgc aag gac atg agc gat gaa gtt				817
Arg Gln Cys Asp Arg Glu Tyr Asp Cys Lys Asp Met Ser Asp Glu Val				
	255	260	265	
ggc tgc gtt aat gtg aca ctc tgc gag gga ccc aac aag ttc aag tgt				865
Gly Cys Val Asn Val Thr Leu Cys Glu Gly Pro Asn Lys Phe Lys Cys				
	270	275	280	
cac agc ggc gaa tgc atc acc ctg gac aaa gtc tgc aac atg gct aga				913
His Ser Gly Glu Cys Ile Thr Leu Asp Lys Val Cys Asn Met Ala Arg				
	285	290	295	300

B
cont.

gac tgc cgg gac tgg tca gat gaa ccc atc aaa gag tgc ggg acc aac 961
 Asp Cys Arg Asp Trp Ser Asp Glu Pro Ile Lys Glu Cys Gly Thr Asn
 305 310 315

gaa tgc ttg gac aac aac ggc ggc tgt tcc cac gtc tgc aat gac ctt 1009
 Glu Cys Leu Asp Asn Asn Gly Gly Cys Ser His Val Cys Asn Asp Leu
 320 325 330

aag atc ggc tac gag tgc ctg tgc ccc gac ggc ttc cag ctg gtg gcc 1057
 Lys Ile Gly Tyr Glu Cys Leu Cys Pro Asp Gly Phe Gln Leu Val Ala
 335 340 345

cag cga aga tgc gaa gat atc gat gag tgt cag gat ccc gac acc tgc 1105
 Gln Arg Arg Cys Glu Asp Ile Asp Glu Cys Gln Asp Pro Asp Thr Cys
 350 355 360

agc cag ctc tgc gtg aac ctg gag ggt ggc tac aag tgc cag tgt gag 1153
 Ser Gln Leu Cys Val Asn Leu Glu Gly Gly Tyr Lys Cys Gln Cys Glu
 365 370 375 380

gaa ggc ttc cag ctg gac ccc cac acg aag gcc tgc aag gct gtg gtc 1201
 Glu Gly Phe Gln Leu Asp Pro His Thr Lys Ala Cys Lys Ala Val Val
 385 390 395

cct gat aaa act gtg aga tgg tgt gca gtg tcg gag cat gag gcc act 1249
 Pro Asp Lys Thr Val Arg Trp Cys Ala Val Ser Glu His Glu Ala Thr
 400 405 410

aag tgc cag agt ttc cgc gac cat atg aaa agc gtc att cca tcc gat 1297
 Lys Cys Gln Ser Phe Arg Asp His Met Lys Ser Val Ile Pro Ser Asp
 415 420 425

ggt ccc agt gtt gct tgt gtg aag aaa gcc tcc tac ctt gat tgc atc 1345
 Gly Pro Ser Val Ala Cys Val Lys Lys Ala Ser Tyr Leu Asp Cys Ile
 430 435 440

agg gcc att gcg gca aac gaa gcg gat gct gtg aca ctg gat gca ggt 1393
 Arg Ala Ile Ala Ala Asn Glu Ala Asp Ala Val Thr Leu Asp Ala Gly
 445 450 455 460

ttg gtg tat gat gct tac ttg gct ccc aat aac ctg aag cct gtg gtg 1441
 Leu Val Tyr Asp Ala Tyr Leu Ala Pro Asn Asn Leu Lys Pro Val Val
 465 470 475

gca gag ttc tat ggg tca aaa gag gat cca cag act ttc tat tat gct 1489
 Ala Glu Phe Tyr Gly Ser Lys Glu Asp Pro Gln Thr Phe Tyr Tyr Ala
 480 485 490

gtt gct gtg gtg aag aag gat agt ggc ttc cag atg aac cag ctt cga 1537
 Val Ala Val Val Lys Lys Asp Ser Gly Phe Gln Met Asn Gln Leu Arg
 495 500 505

ggc aag aag tcc tgc cac acg ggt cta ggc agg tcc gct ggg tgg aac 1585
 Gly Lys Lys Ser Cys His Thr Gly Leu Gly Arg Ser Ala Gly Trp Asn
 510 515 520

B
cont

atc ccc ata ggc tta ctt tac tgt gac tta cct gag cca cgt aaa cct 1633
 Ile Pro Ile Gly Leu Leu Tyr Cys Asp Leu Pro Glu Pro Arg Lys Pro
 525 530 535 540

ctt gag aaa gca gtg gcc aat ttc ttc tcg ggc agc tgt gcc cct tgt 1681
 Leu Glu Lys Ala Val Ala Asn Phe Phe Ser Gly Ser Cys Ala Pro Cys
 545 550 555

gcg gat ggg acg gac ttc ccc cag ctg tgt caa ctg tgt cca ggg tgt 1729
 Ala Asp Gly Thr Asp Phe Pro Gln Leu Cys Gln Leu Cys Pro Gly Cys
 560 565 570

ggc tgc tcc acc ctt aac caa tac ttc ggc tac tcg gga gcc ttc aag 1777
 Gly Cys Ser Thr Leu Asn Gln Tyr Phe Gly Tyr Ser Gly Ala Phe Lys
 575 580 585

tgt ctg aag gat ggt gct ggg gat gtg gcc ttt gtc aag cac tcg act 1825
 Cys Leu Lys Asp Gly Ala Gly Asp Val Ala Phe Val Lys His Ser Thr
 590 595 600

ata ttt gag aac ttg gca aac aag gct gac agg gac cag tat gag ctg 1873
 Ile Phe Glu Asn Leu Ala Asn Lys Ala Asp Arg Asp Gln Tyr Glu Leu
 605 610 615 620

ctt tgc cta gac aac acc cgg aag ccg gta gat gaa tac aag gac tgc 1921
 Leu Cys Leu Asp Asn Thr Arg Lys Pro Val Asp Glu Tyr Lys Asp Cys
 625 630 635

cac ttg gcc cag gtc cct tct cat acc gtc gtg gcc cga agt atg ggc 1969
 His Leu Ala Gln Val Pro Ser His Thr Val Val Ala Arg Ser Met Gly
 640 645 650

ggc aag gag gac ttg atc tgg gag ctt ctc aac cag gcc cag gaa cat 2017
 Gly Lys Glu Asp Leu Ile Trp Glu Leu Leu Asn Gln Ala Gln Glu His
 655 660 665

ttt ggc aaa gac aaa tca aaa gaa ttc caa cta ttc agc tct cct cat 2065
 Phe Gly Lys Asp Lys Ser Lys Glu Phe Gln Leu Phe Ser Ser Pro His
 670 675 680

ggg aag gac ctg ctg ttt aag gac tct gcc cac ggg ttt tta aaa gtc 2113
 Gly Lys Asp Leu Leu Phe Lys Asp Ser Ala His Gly Phe Leu Lys Val
 685 690 695 700

ccc cca agg atg gat gcc aag atg tac ctg ggc tat gag tat gtc act 2161
 Pro Pro Arg Met Asp Ala Lys Met Tyr Leu Gly Tyr Glu Tyr Val Thr
 705 710 715

gcc atc cgg aat cta cgg gaa ggc aca tgc cca gaa gcc cca aca gat 2209
 Ala Ile Arg Asn Leu Arg Glu Gly Thr Cys Pro Glu Ala Pro Thr Asp
 720 725 730

gaa tgc aag cct gtg aag tgg tgt gcg ctg agc cac cac gag agg ctc 2257
 Glu Cys Lys Pro Val Lys Trp Cys Ala Leu Ser His His Glu Arg Leu
 735 740 745

aag tgt gat gag tgg agt gtt aac agt gta ggg aaa ata gag tgt gta 2305

B
cont.

Lys	Cys	Asp	Glu	Trp	Ser	Val	Asn	Ser	Val	Gly	Lys	Ile	Glu	Cys	Val		
750						755					760						
tca	gca	gag	acc	acc	gaa	gac	tgc	atc	gcc	aag	atc	atg	aat	gga	gaa	2353	
Ser	Ala	Glu	Thr	Thr	Glu	Asp	Cys	Ile	Ala	Lys	Ile	Met	Asn	Gly	Glu		
765					770				775					780			
gct	gat	gcc	atg	agc	ttg	gat	gga	ggg	ttt	gtc	tac	ata	gcg	ggc	aag	2401	
Ala	Asp	Ala	Met	Ser	Leu	Asp	Gly	Gly	Phe	Val	Tyr	Ile	Ala	Gly	Lys		
				785					790					795			
tgt	ggc	ctg	gtg	cct	gtc	ttg	gca	gaa	aac	tac	aat	aag	agc	gat	aat	2449	
Cys	Gly	Leu	Val	Pro	Val	Leu	Ala	Glu	Asn	Tyr	Asn	Lys	Ser	Asp	Asn		
			800					805					810				
tgt	gag	gat	aca	cca	gag	gca	ggg	tat	ttt	gct	gta	gca	gtg	gtg	aag	2497	
Cys	Glu	Asp	Thr	Pro	Glu	Ala	Gly	Tyr	Phe	Ala	Val	Ala	Val	Val	Lys		
			815				820					825					
aaa	tca	gct	tct	gac	ctc	acc	tgg	gac	aat	ctg	aaa	ggc	aag	aag	tcc	2545	
Lys	Ser	Ala	Ser	Asp	Leu	Thr	Trp	Asp	Asn	Leu	Lys	Gly	Lys	Lys	Ser		
			830			835					840						
tgc	cat	acg	gca	gtt	ggc	aga	acc	gct	ggc	tgg	aac	atc	ccc	atg	ggc	2593	
Cys	His	Thr	Ala	Val	Gly	Arg	Thr	Ala	Gly	Trp	Asn	Ile	Pro	Met	Gly		
845					850				855					860			
ctg	ctc	tac	aat	aag	atc	aac	cac	tgc	aga	ttt	gat	gaa	ttt	ttc	agt	2641	
Leu	Leu	Tyr	Asn	Lys	Ile	Asn	His	Cys	Arg	Phe	Asp	Glu	Phe	Phe	Ser		
			865					870						875			
gaa	ggc	tgt	gcc	cct	ggg	tct	aag	aaa	gac	tcc	agt	ctc	tgt	aag	ctg	2689	
Glu	Gly	Cys	Ala	Pro	Gly	Ser	Lys	Lys	Asp	Ser	Ser	Leu	Cys	Lys	Leu		
			880					885					890				
tgt	atg	ggc	tca	ggc	cta	aac	ctg	tgt	gaa	ccc	aac	aac	aaa	gag	gga	2737	
Cys	Met	Gly	Ser	Gly	Leu	Asn	Leu	Cys	Glu	Pro	Asn	Asn	Lys	Glu	Gly		
			895			900						905					
tac	tac	ggc	tac	aca	ggc	gct	ttc	agg	tgt	ctg	gtt	gag	aag	gga	gat	2785	
Tyr	Tyr	Gly	Tyr	Thr	Gly	Ala	Phe	Arg	Cys	Leu	Val	Glu	Lys	Gly	Asp		
			910			915					920						
gtg	gcc	ttt	gtg	aaa	cac	cag	act	gtc	cca	cag	aac	act	ggg	gga	aaa	2833	
Val	Ala	Phe	Val	Lys	His	Gln	Thr	Val	Pro	Gln	Asn	Thr	Gly	Gly	Lys		
925					930					935				940			
aac	cct	gat	cca	tgg	gct	aag	aat	ctg	aat	gaa	aaa	gac	tat	gag	ttg	2881	
Asn	Pro	Asp	Pro	Trp	Ala	Lys	Asn	Leu	Asn	Glu	Lys	Asp	Tyr	Glu	Leu		
				945				950						955			
ctg	tgc	ctt	gat	ggc	acc	agg	aaa	cct	gtg	gag	gag	tat	gcg	aac	tgc	2929	
Leu	Cys	Leu	Asp	Gly	Thr	Arg	Lys	Pro	Val	Glu	Glu	Tyr	Ala	Asn	Cys		
			960					965					970				
cac	ctg	gcc	aga	gcc	ccg	aat	cac	gct	gtg	gtc	aca	cgg	aaa	gat	aag	2977	
His	Leu	Ala	Arg	Ala	Pro	Asn	His	Ala	Val	Val	Thr	Arg	Lys	Asp	Lys		

B
Cont.

975	980	985	
gaa gct tgc gtc cac aag ata tta cgt caa cag cag cac cta ttt gga			3025
Glu Ala Cys Val His Lys Ile Leu Arg Gln Gln Gln His Leu Phe Gly			
990	995	1000	
agc aac gta act gac tgc tcg ggc aac ttt tgt ttg ttc cgg tcg gaa			3073
Ser Asn Val Thr Asp Cys Ser Gly Asn Phe Cys Leu Phe Arg Ser Glu			
1005	1010	1015	1020
acc aag gac ctt ctg ttc aga gat gac aca gta tgt ttg gcc aaa ctt			3121
Thr Lys Asp Leu Leu Phe Arg Asp Asp Thr Val Cys Leu Ala Lys Leu			
	1025	1030	1035
cat gac aga aac aca tat gaa aaa tac tta gga gaa gaa tat gtc aag			3169
His Asp Arg Asn Thr Tyr Glu Lys Tyr Leu Gly Glu Glu Tyr Val Lys			
	1040	1045	1050
gct gtt ggt aac ctg aga aaa tgc tcc acc tca tca ctc ctg gaa gcc			3217
Ala Val Gly Asn Leu Arg Lys Cys Ser Thr Ser Ser Leu Leu Glu Ala			
	1055	1060	1065
tgc act ttc cgt aga cct taaaatctca gaggtagggc tgccaccaag			3265
Cys Thr Phe Arg Arg Pro			
1070			
gtgaagatgg gaacgcagat gatccatgag tttgccctgg ttctactggc ccaagtgggt			3325
tgtgctaacc acgtctgtct tcacagctct gtgttgccat gtgtgctgaa caaaaaataa			3385
aaattattat tgattttata tttcgggggg ggggctgcag ccc			3428
<210> 2			
<211> 1074			
<212> PRT			
<213> Homo sapiens			
<400> 2			
Met Gly Pro Trp Gly Trp Lys Leu Arg Trp Thr Val Ala Leu Leu Leu			
1 5 10 15			
Ala Ala Ala Gly Thr Ala Val Gly Asp Arg Cys Glu Arg Asn Glu Phe			
20 25 30			
Gln Cys Gln Asp Gly Lys Cys Ile Ser Tyr Lys Trp Val Cys Asp Gly			
35 40 45			
Ser Ala Glu Cys Gln Asp Gly Ser Asp Glu Ser Gln Glu Thr Cys Leu			
50 55 60			
Ser Val Thr Cys Lys Ser Gly Asp Phe Ser Cys Gly Gly Arg Val Asn			
65 70 75 80			
Arg Cys Ile Pro Gln Phe Trp Arg Cys Asp Gly Gln Val Asp Cys Asp			
85 90 95			
Asn Gly Ser Asp Glu Gln Gly Cys Pro Pro Lys Thr Cys Ser Gln Asp			
100 105 110			
Glu Phe Arg Cys His Asp Gly Lys Cys Ile Ser Arg Gln Phe Val Cys			
115 120 125			
Asp Ser Asp Arg Asp Cys Leu Asp Gly Ser Asp Glu Ala Ser Cys Pro			
130 135 140			
Val Leu Thr Cys Gly Pro Ala Ser Phe Gln Cys Asn Ser Ser Thr Cys			
145 150 155 160			
Ile Pro Gln Leu Trp Ala Cys Asp Asn Asp Pro Asp Cys Glu Asp Gly			

				165					170					175			
Ser	Asp	Glu	Trp	Pro	Gln	Arg	Cys	Arg	Gly	Leu	Tyr	Val	Phe	Gln	Gly		
				180					185					190			
Asp	Ser	Ser	Pro	Cys	Ser	Ala	Phe	Glu	Phe	His	Cys	Leu	Ser	Gly	Glu		
		195					200						205				
Cys	Ile	His	Ser	Ser	Trp	Arg	Cys	Asp	Gly	Gly	Pro	Asp	Cys	Lys	Asp		
	210					215					220						
Lys	Ser	Asp	Glu	Glu	Asn	Cys	Ala	Val	Ala	Thr	Cys	Arg	Pro	Asp	Glu		
	225				230					235					240		
Phe	Gln	Cys	Ser	Asp	Gly	Asn	Cys	Ile	His	Gly	Ser	Arg	Gln	Cys	Asp		
				245					250					255			
Arg	Glu	Tyr	Asp	Cys	Lys	Asp	Met	Ser	Asp	Glu	Val	Gly	Cys	Val	Asn		
		260						265					270				
Val	Thr	Leu	Cys	Glu	Gly	Pro	Asn	Lys	Phe	Lys	Cys	His	Ser	Gly	Glu		
	275						280					285					
Cys	Ile	Thr	Leu	Asp	Lys	Val	Cys	Asn	Met	Ala	Arg	Asp	Cys	Arg	Asp		
	290				295					300							
Trp	Ser	Asp	Glu	Pro	Ile	Lys	Glu	Cys	Gly	Thr	Asn	Glu	Cys	Leu	Asp		
	305				310					315					320		
Asn	Asn	Gly	Gly	Cys	Ser	His	Val	Cys	Asn	Asp	Leu	Lys	Ile	Gly	Tyr		
				325					330					335			
Glu	Cys	Leu	Cys	Pro	Asp	Gly	Phe	Gln	Leu	Val	Ala	Gln	Arg	Arg	Cys		
		340						345					350				
Glu	Asp	Ile	Asp	Glu	Cys	Gln	Asp	Pro	Asp	Thr	Cys	Ser	Gln	Leu	Cys		
	355						360					365					
Val	Asn	Leu	Glu	Gly	Gly	Tyr	Lys	Cys	Gln	Cys	Glu	Glu	Gly	Phe	Gln		
	370					375					380						
Leu	Asp	Pro	His	Thr	Lys	Ala	Cys	Lys	Ala	Val	Val	Pro	Asp	Lys	Thr		
	385				390					395					400		
Val	Arg	Trp	Cys	Ala	Val	Ser	Glu	His	Glu	Ala	Thr	Lys	Cys	Gln	Ser		
			405						410					415			
Phe	Arg	Asp	His	Met	Lys	Ser	Val	Ile	Pro	Ser	Asp	Gly	Pro	Ser	Val		
		420						425				430					
Ala	Cys	Val	Lys	Lys	Ala	Ser	Tyr	Leu	Asp	Cys	Ile	Arg	Ala	Ile	Ala		
		435					440					445					
Ala	Asn	Glu	Ala	Asp	Ala	Val	Thr	Leu	Asp	Ala	Gly	Leu	Val	Tyr	Asp		
	450					455					460						
Ala	Tyr	Leu	Ala	Pro	Asn	Asn	Leu	Lys	Pro	Val	Val	Ala	Glu	Phe	Tyr		
	465				470					475					480		
Gly	Ser	Lys	Glu	Asp	Pro	Gln	Thr	Phe	Tyr	Tyr	Ala	Val	Ala	Val	Val		
			485						490					495			
Lys	Lys	Asp	Ser	Gly	Phe	Gln	Met	Asn	Gln	Leu	Arg	Gly	Lys	Lys	Ser		
		500						505					510				
Cys	His	Thr	Gly	Leu	Gly	Arg	Ser	Ala	Gly	Trp	Asn	Ile	Pro	Ile	Gly		
		515					520					525					
Leu	Leu	Tyr	Cys	Asp	Leu	Pro	Glu	Pro	Arg	Lys	Pro	Leu	Glu	Lys	Ala		
	530					535					540						
Val	Ala	Asn	Phe	Phe	Ser	Gly	Ser	Cys	Ala	Pro	Cys	Ala	Asp	Gly	Thr		
	545				550					555					560		
Asp	Phe	Pro	Gln	Leu	Cys	Gln	Leu	Cys	Pro	Gly	Cys	Gly	Cys	Ser	Thr		
			565						570					575			
Leu	Asn	Gln	Tyr	Phe	Gly	Tyr	Ser	Gly	Ala	Phe	Lys	Cys	Leu	Lys	Asp		
		580						585					590				
Gly	Ala	Gly	Asp	Val	Ala	Phe	Val	Lys	His	Ser	Thr	Ile	Phe	Glu	Asn		
	595					600						605					
Leu	Ala	Asn	Lys	Ala	Asp	Arg	Asp	Gln	Tyr	Glu	Leu	Leu	Cys	Leu	Asp		
	610					615					620						

Asn	Thr	Arg	Lys	Pro	Val	Asp	Glu	Tyr	Lys	Asp	Cys	His	Leu	Ala	Gln	625	630	635	640
Val	Pro	Ser	His	Thr	Val	Val	Ala	Arg	Ser	Met	Gly	Gly	Lys	Glu	Asp	645	650	655	
Leu	Ile	Trp	Glu	Leu	Leu	Asn	Gln	Ala	Gln	Glu	His	Phe	Gly	Lys	Asp	660	665	670	
Lys	Ser	Lys	Glu	Phe	Gln	Leu	Phe	Ser	Ser	Pro	His	Gly	Lys	Asp	Leu	675	680	685	
Leu	Phe	Lys	Asp	Ser	Ala	His	Gly	Phe	Leu	Lys	Val	Pro	Pro	Arg	Met	690	695	700	
Asp	Ala	Lys	Met	Tyr	Leu	Gly	Tyr	Glu	Tyr	Val	Thr	Ala	Ile	Arg	Asn	705	710	715	720
Leu	Arg	Glu	Gly	Thr	Cys	Pro	Glu	Ala	Pro	Thr	Asp	Glu	Cys	Lys	Pro	725	730	735	
Val	Lys	Trp	Cys	Ala	Leu	Ser	His	His	Glu	Arg	Leu	Lys	Cys	Asp	Glu	740	745	750	
Trp	Ser	Val	Asn	Ser	Val	Gly	Lys	Ile	Glu	Cys	Val	Ser	Ala	Glu	Thr	755	760	765	
Thr	Glu	Asp	Cys	Ile	Ala	Lys	Ile	Met	Asn	Gly	Glu	Ala	Asp	Ala	Met	770	775	780	
Ser	Leu	Asp	Gly	Gly	Phe	Val	Tyr	Ile	Ala	Gly	Lys	Cys	Gly	Leu	Val	785	790	795	800
Pro	Val	Leu	Ala	Glu	Asn	Tyr	Asn	Lys	Ser	Asp	Asn	Cys	Glu	Asp	Thr	805	810	815	
Pro	Glu	Ala	Gly	Tyr	Phe	Ala	Val	Ala	Val	Val	Lys	Lys	Ser	Ala	Ser	820	825	830	
Asp	Leu	Thr	Trp	Asp	Asn	Leu	Lys	Gly	Lys	Lys	Ser	Cys	His	Thr	Ala	835	840	845	
Val	Gly	Arg	Thr	Ala	Gly	Trp	Asn	Ile	Pro	Met	Gly	Leu	Leu	Tyr	Asn	850	855	860	
Lys	Ile	Asn	His	Cys	Arg	Phe	Asp	Glu	Phe	Phe	Ser	Glu	Gly	Cys	Ala	865	870	875	880
Pro	Gly	Ser	Lys	Lys	Asp	Ser	Ser	Leu	Cys	Lys	Leu	Cys	Met	Gly	Ser	885	890	895	
Gly	Leu	Asn	Leu	Cys	Glu	Pro	Asn	Asn	Lys	Glu	Gly	Tyr	Tyr	Gly	Tyr	900	905	910	
Thr	Gly	Ala	Phe	Arg	Cys	Leu	Val	Glu	Lys	Gly	Asp	Val	Ala	Phe	Val	915	920	925	
Lys	His	Gln	Thr	Val	Pro	Gln	Asn	Thr	Gly	Gly	Lys	Asn	Pro	Asp	Pro	930	935	940	
Trp	Ala	Lys	Asn	Leu	Asn	Glu	Lys	Asp	Tyr	Glu	Leu	Leu	Cys	Leu	Asp	945	950	955	960
Gly	Thr	Arg	Lys	Pro	Val	Glu	Glu	Tyr	Ala	Asn	Cys	His	Leu	Ala	Arg	965	970	975	
Ala	Pro	Asn	His	Ala	Val	Val	Thr	Arg	Lys	Asp	Lys	Glu	Ala	Cys	Val	980	985	990	
His	Lys	Ile	Leu	Arg	Gln	Gln	Gln	His	Leu	Phe	Gly	Ser	Asn	Val	Thr	995	1000	1005	
Asp	Cys	Ser	Gly	Asn	Phe	Cys	Leu	Phe	Arg	Ser	Glu	Thr	Lys	Asp	Leu	1010	1015	1020	
Leu	Phe	Arg	Asp	Asp	Thr	Val	Cys	Leu	Ala	Lys	Leu	His	Asp	Arg	Asn	1025	1030	1035	1040
Thr	Tyr	Glu	Lys	Tyr	Leu	Gly	Glu	Glu	Tyr	Val	Lys	Ala	Val	Gly	Asn	1045	1050	1055	
Leu	Arg	Lys	Cys	Ser	Thr	Ser	Ser	Leu	Leu	Glu	Ala	Cys	Thr	Phe	Arg	1060	1065	1070	
Arg	Pro																		

<210> 3
 <211> 4603
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (14)...(4243)

<400> 3
 agaggctgcg agc atg ggg ccc tgg ggc tgg aaa ttg cgc tgg acc gtc 49
 Met Gly Pro Trp Gly Trp Lys Leu Arg Trp Thr Val
 1 5 10

gcc ttg ctc ctc gcc gcg gcg ggg act gca gtg ggc gac aga tgt gaa 97
 Ala Leu Leu Leu Ala Ala Ala Gly Thr Ala Val Gly Asp Arg Cys Glu
 15 20 25

aga aac gag ttc cag tgc caa gac ggg aaa tgc atc tcc tac aag tgg 145
 Arg Asn Glu Phe Gln Cys Gln Asp Gly Lys Cys Ile Ser Tyr Lys Trp
 30 35 40

gtc tgc gat ggc agc gct gag tgc cag gat ggc tct gat gag tcc cag 193
 Val Cys Asp Gly Ser Ala Glu Cys Gln Asp Gly Ser Asp Glu Ser Gln
 45 50 55 60

gag acg tgc ttg tct gtc acc tgc aaa tcc ggg gac ttc agc tgt ggg 241
 Glu Thr Cys Leu Ser Val Thr Cys Lys Ser Gly Asp Phe Ser Cys Gly
 65 70 75

ggc cgt gtc aac cgc tgc att cct cag ttc tgg agg tgc gat ggc caa 289
 Gly Arg Val Asn Arg Cys Ile Pro Gln Phe Trp Arg Cys Asp Gly Gln
 80 85 90

gtg gac tgc gac aac ggc tca gac gag caa ggc tgt ccc ccc aag acg 337
 Val Asp Cys Asp Asn Gly Ser Asp Glu Gln Gly Cys Pro Pro Lys Thr
 95 100 105

tgc tcc cag gac gag ttt cgc tgc cac gat ggg aag tgc atc tct cgg 385
 Cys Ser Gln Asp Glu Phe Arg Cys His Asp Gly Lys Cys Ile Ser Arg
 110 115 120

cag ttc gtc tgt gac tca gac cgg gac tgc ttg gac ggc tca gac gag 433
 Gln Phe Val Cys Asp Ser Asp Arg Asp Cys Leu Asp Gly Ser Asp Glu
 125 130 135 140

gcc tcc tgc ccg gtg ctc acc tgt ggt ccc gcc agc ttc cag tgc aac 481
 Ala Ser Cys Pro Val Leu Thr Cys Gly Pro Ala Ser Phe Gln Cys Asn
 145 150 155

agc tcc acc tgc atc ccc cag ctg tgg gcc tgc gac aac gac ccc gac 529
 Ser Ser Thr Cys Ile Pro Gln Leu Trp Ala Cys Asp Asn Asp Pro Asp
 160 165 170

tgc gaa gat ggc tcg gat gag tgg ccg cag cgc tgt agg ggt ctt tac 577

Cys	Glu	Asp	Gly	Ser	Asp	Glu	Trp	Pro	Gln	Arg	Cys	Arg	Gly	Leu	Tyr	
		175					180					185				
gtg	ttc	caa	ggg	gac	agt	agc	ccc	tgc	tcg	gcc	ttc	gag	ttc	cac	tgc	625
Val	Phe	Gln	Gly	Asp	Ser	Ser	Pro	Cys	Ser	Ala	Phe	Glu	Phe	His	Cys	
	190					195				200						
cta	agt	ggc	gag	tgc	atc	cac	tcc	agc	tgg	cgc	tgt	gat	ggt	ggc	ccc	673
Leu	Ser	Gly	Glu	Cys	Ile	His	Ser	Ser	Trp	Arg	Cys	Asp	Gly	Gly	Pro	
205					210					215					220	
gac	tgc	aag	gac	aaa	tct	gac	gag	gaa	aac	tgc	gct	gtg	gcc	acc	tgt	721
Asp	Cys	Lys	Asp	Lys	Ser	Asp	Glu	Glu	Asn	Cys	Ala	Val	Ala	Thr	Cys	
				225					230					235		
cgc	cct	gac	gaa	ttc	cag	tgc	tct	gat	gga	aac	tgc	atc	cat	ggc	agc	769
Arg	Pro	Asp	Glu	Phe	Gln	Cys	Ser	Asp	Gly	Asn	Cys	Ile	His	Gly	Ser	
		240						245					250			
cgg	cag	tgt	gac	cgg	gaa	tat	gac	tgc	aag	gac	atg	agc	gat	gaa	gtt	817
Arg	Gln	Cys	Asp	Arg	Glu	Tyr	Asp	Cys	Lys	Asp	Met	Ser	Asp	Glu	Val	
		255					260				265					
ggc	tgc	gtt	aat	gtg	aca	ctc	tgc	gag	gga	ccc	aac	aag	ttc	aag	tgt	865
Gly	Cys	Val	Asn	Val	Thr	Leu	Cys	Glu	Gly	Pro	Asn	Lys	Phe	Lys	Cys	
	270					275				280						
cac	agc	ggc	gaa	tgc	atc	acc	ctg	gac	aaa	gtc	tgc	aac	atg	gct	aga	913
His	Ser	Gly	Glu	Cys	Ile	Thr	Leu	Asp	Lys	Val	Cys	Asn	Met	Ala	Arg	
285					290					295					300	
gac	tgc	cgg	gac	tgg	tca	gat	gaa	ccc	atc	aaa	gag	tgc	ggg	acc	aac	961
Asp	Cys	Arg	Asp	Trp	Ser	Asp	Glu	Pro	Ile	Lys	Glu	Cys	Gly	Thr	Asn	
				305					310					315		
gaa	tgc	ttg	gac	aac	aac	ggc	ggc	tgt	tcc	cac	gtc	tgc	aat	gac	ctt	1009
Glu	Cys	Leu	Asp	Asn	Asn	Gly	Gly	Cys	Ser	His	Val	Cys	Asn	Asp	Leu	
			320					325					330			
aag	atc	ggc	tac	gag	tgc	ctg	tgc	ccc	gac	ggc	ttc	cag	ctg	gtg	gcc	1057
Lys	Ile	Gly	Tyr	Glu	Cys	Leu	Cys	Pro	Asp	Gly	Phe	Gln	Leu	Val	Ala	
		335					340					345				
cag	cga	aga	tgc	gaa	gat	atc	gat	gag	tgt	cag	gat	ccc	gac	acc	tgc	1105
Gln	Arg	Arg	Cys	Glu	Asp	Ile	Asp	Glu	Cys	Gln	Asp	Pro	Asp	Thr	Cys	
		350				355					360					
agc	cag	ctc	tgc	gtg	aac	ctg	gag	ggt	ggc	tac	aag	tgc	cag	tgt	gag	1153
Ser	Gln	Leu	Cys	Val	Asn	Leu	Glu	Gly	Gly	Tyr	Lys	Cys	Gln	Cys	Glu	
365					370					375					380	
gaa	ggc	ttc	cag	ctg	gac	ccc	cac	acg	aag	gcc	tgc	aag	gct	gtg	ggc	1201
Glu	Gly	Phe	Gln	Leu	Asp	Pro	His	Thr	Lys	Ala	Cys	Lys	Ala	Val	Gly	
				385					390					395		
tcc	atc	gcc	tac	ctc	ttc	ttc	acc	aac	cgg	cac	gag	gtc	agg	aag	atg	1249
Ser	Ile	Ala	Tyr	Leu	Phe	Phe	Thr	Asn	Arg	His	Glu	Val	Arg	Lys	Met	

400								405				410				
acg	ctg	gac	cgg	agc	gag	tac	acc	agc	ctc	atc	ccc	aac	ctg	agg	aac	1297
Thr	Leu	Asp	Arg	Ser	Glu	Tyr	Thr	Ser	Leu	Ile	Pro	Asn	Leu	Arg	Asn	
		415					420					425				
gtg	gtc	gct	ctg	gac	acg	gag	gtg	gcc	agc	aat	aga	atc	tac	tggtct		1345
Val	Val	Ala	Leu	Asp	Thr	Glu	Val	Ala	Ser	Asn	Arg	Ile	Tyr	Trp	Ser	
	430					435					440					
gac	ctg	tcc	cag	aga	atg	atc	tgc	agc	acc	cag	ctt	gac	aga	gcc	cac	1393
Asp	Leu	Ser	Gln	Arg	Met	Ile	Cys	Ser	Thr	Gln	Leu	Asp	Arg	Ala	His	
445					450					455					460	
ggc	gtc	tct	tcc	tat	gac	acc	gtc	atc	agc	agg	gac	atc	cag	gcc	ccc	1441
Gly	Val	Ser	Ser	Tyr	Asp	Thr	Val	Ile	Ser	Arg	Asp	Ile	Gln	Ala	Pro	
				465					470					475		
gac	ggg	ctg	gct	gtg	gac	tgg	atc	cac	agc	aac	atc	tac	tgg	acc	gac	1489
Asp	Gly	Leu	Ala	Val	Asp	Trp	Ile	His	Ser	Asn	Ile	Tyr	Trp	Thr	Asp	
			480					485					490			
tct	gtc	ctg	ggc	act	gtc	tct	gtt	gcg	gat	acc	aag	ggc	gtg	aag	agg	1537
Ser	Val	Leu	Gly	Thr	Val	Ser	Val	Ala	Asp	Thr	Lys	Gly	Val	Lys	Arg	
		495					500					505				
aaa	acg	tta	ttc	agg	gag	aac	ggc	tcc	aag	cca	agg	gcc	atc	gtg	gtg	1585
Lys	Thr	Leu	Phe	Arg	Glu	Asn	Gly	Ser	Lys	Pro	Arg	Ala	Ile	Val	Val	
	510					515					520					
gat	cct	gtt	cat	ggc	ttc	atg	tac	tgg	act	gac	tgg	gga	act	ccc	gcc	1633
Asp	Pro	Val	His	Gly	Phe	Met	Tyr	Trp	Thr	Asp	Trp	Gly	Thr	Pro	Ala	
525					530					535					540	
aag	atc	aag	aaa	ggg	ggc	ctg	aat	ggt	gtg	gac	atc	tac	tcg	ctg	gtg	1681
Lys	Ile	Lys	Lys	Gly	Gly	Leu	Asn	Gly	Val	Asp	Ile	Tyr	Ser	Leu	Val	
				545					550					555		
act	gaa	aac	att	cag	tgg	ccc	aat	ggc	atc	acc	cta	gat	ctc	ctc	agt	1729
Thr	Glu	Asn	Ile	Gln	Trp	Pro	Asn	Gly	Ile	Thr	Leu	Asp	Leu	Leu	Ser	
			560					565					570			
ggc	cgc	ctc	tac	tgg	gtt	gac	tcc	aaa	ctt	cac	tcc	atc	tca	agc	atc	1777
Gly	Arg	Leu	Tyr	Trp	Val	Asp	Ser	Lys	Leu	His	Ser	Ile	Ser	Ser	Ile	
		575					580					585				
gat	gtc	aat	ggg	ggc	aac	cgg	aag	acc	atc	ttg	gag	gat	gaa	aag	agg	1825
Asp	Val	Asn	Gly	Gly	Asn	Arg	Lys	Thr	Ile	Leu	Glu	Asp	Glu	Lys	Arg	
	590					595					600					
ctg	gcc	cac	ccc	ttc	tcc	ttg	gcc	gtc	ttt	gag	gac	aaa	gta	ttt	tggt	1873
Leu	Ala	His	Pro	Phe	Ser	Leu	Ala	Val	Phe	Glu	Asp	Lys	Val	Phe	Trp	
605					610				615						620	
aca	gat	atc	atc	aac	gaa	gcc	att	ttc	agt	gcc	aac	cgc	ctc	aca	ggt	1921
Thr	Asp	Ile	Ile	Asn	Glu	Ala	Ile	Phe	Ser	Ala	Asn	Arg	Leu	Thr	Gly	
				625					630						635	

tcc gat gtc aac ttg ttg gct gaa aac cta ctg tcc cca gag gat atg	1969
Ser Asp Val Asn Leu Leu Ala Glu Asn Leu Leu Ser Pro Glu Asp Met	
640 645 650	
gtc ctc ttc cac aac ctc acc cag cca aga gga gtg aac tgg tgt gag	2017
Val Leu Phe His Asn Leu Thr Gln Pro Arg Gly Val Asn Trp Cys Glu	
655 660 665	
agg acc acc ctg agc aat ggc ggc tgc cag tat ctg tgc ctc cct gcc	2065
Arg Thr Thr Leu Ser Asn Gly Gly Cys Gln Tyr Leu Cys Leu Pro Ala	
670 675 680	
ccg cag atc aac ccc cac tcg ccc aag ttt acc tgc gcc tgc ccg gac	2113
Pro Gln Ile Asn Pro His Ser Pro Lys Phe Thr Cys Ala Cys Pro Asp	
685 690 695 700	
ggc atg ctg ctg gcc agg gac atg agg agc tgc ctc aca gag gct gag	2161
Gly Met Leu Leu Ala Arg Asp Met Arg Ser Cys Leu Thr Glu Ala Glu	
705 710 715	
gct gca gtg gcc acc cag gag aca tcc acc gtc agg cta aag gtc gtc	2209
Ala Ala Val Ala Thr Gln Glu Thr Ser Thr Val Arg Leu Lys Val Val	
720 725 730	
cct gat aaa act gtg aga tgg tgt gca gtg tcg gag cat gag gcc act	2257
Pro Asp Lys Thr Val Arg Trp Cys Ala Val Ser Glu His Glu Ala Thr	
735 740 745	
aag tgc cag agt ttc cgc gac cat atg aaa agc gtc att cca tcc gat	2305
Lys Cys Gln Ser Phe Arg Asp His Met Lys Ser Val Ile Pro Ser Asp	
750 755 760	
ggc ccc agt gtt gct tgt gtg aag aaa gcc tcc tac ctt gat tgc atc	2353
Gly Pro Ser Val Ala Cys Val Lys Lys Ala Ser Tyr Leu Asp Cys Ile	
765 770 775 780	
agg gcc att gcg gca aac gaa gcg gat gct gtg aca ctg gat gca ggt	2401
Arg Ala Ile Ala Ala Asn Glu Ala Asp Ala Val Thr Leu Asp Ala Gly	
785 790 795	
ttg gtg tat gat gct tac ttg gct ccc aat aac ctg aag cct gtg gtg	2449
Leu Val Tyr Asp Ala Tyr Leu Ala Pro Asn Asn Leu Lys Pro Val Val	
800 805 810	
gca gag ttc tat ggg tca aaa gag gat cca cag act ttc tat tat gct	2497
Ala Glu Phe Tyr Gly Ser Lys Glu Asp Pro Gln Thr Phe Tyr Tyr Ala	
815 820 825	
gtt gct gtg gtg aag aag gat agt ggc ttc cag atg aac cag ctt cga	2545
Val Ala Val Val Lys Lys Asp Ser Gly Phe Gln Met Asn Gln Leu Arg	
830 835 840	
ggc aag aag tcc tgc cac acg ggt cta ggc agg tcc gct ggg tgg aac	2593
Gly Lys Lys Ser Cys His Thr Gly Leu Gly Arg Ser Ala Gly Trp Asn	
845 850 855 860	

atc ccc ata ggc tta ctt tac tgt gac tta cct gag cca cgt aaa cct Ile Pro Ile Gly Leu Leu Tyr Cys Asp Leu Pro Glu Pro Arg Lys Pro 865 870 875	2641
ctt gag aaa gca gtg gcc aat ttc ttc tcg ggc agc tgt gcc cct tgt Leu Glu Lys Ala Val Ala Asn Phe Phe Ser Gly Ser Cys Ala Pro Cys 880 885 890	2689
gcg gat ggg acg gac ttc ccc cag ctg tgt caa ctg tgt cca ggg tgt Ala Asp Gly Thr Asp Phe Pro Gln Leu Cys Gln Leu Cys Pro Gly Cys 895 900 905	2737
ggc tgc tcc acc ctt aac caa tac ttc ggc tac tcg gga gcc ttc aag Gly Cys Ser Thr Leu Asn Gln Tyr Phe Gly Tyr Ser Gly Ala Phe Lys 910 915 920	2785
tgt ctg aag gat ggt gct ggg gat gtg gcc ttt gtc aag cac tcg act Cys Leu Lys Asp Gly Ala Gly Asp Val Ala Phe Val Lys His Ser Thr 925 930 935 940	2833
ata ttt gag aac ttg gca aac aag gct gac agg gac cag tat gag ctg Ile Phe Glu Asn Leu Ala Asn Lys Ala Asp Arg Asp Gln Tyr Glu Leu 945 950 955	2881
ctt tgc cta gac aac acc cgg aag ccg gta gat gaa tac aag gac tgc Leu Cys Leu Asp Asn Thr Arg Lys Pro Val Asp Glu Tyr Lys Asp Cys 960 965 970	2929
cac ttg gcc cag gtc cct tct cat acc gtc gtg gcc cga agt atg ggc His Leu Ala Gln Val Pro Ser His Thr Val Val Ala Arg Ser Met Gly 975 980 985	2977
ggc aag gag gac ttg atc tgg gag ctt ctc aac cag gcc cag gaa cat Gly Lys Glu Asp Leu Ile Trp Glu Leu Leu Asn Gln Ala Gln Glu His 990 995 1000	3025
ttt ggc aaa gac aaa tca aaa gaa ttc caa cta ttc agc tct cct cat Phe Gly Lys Asp Lys Ser Lys Glu Phe Gln Leu Phe Ser Ser Pro His 1005 1010 1015 1020	3073
ggg aag gac ctg ctg ttt aag gac tct gcc cac ggg ttt tta aaa gtc Gly Lys Asp Leu Leu Phe Lys Asp Ser Ala His Gly Phe Leu Lys Val 1025 1030 1035	3121
ccc cca agg atg gat gcc aag atg tac ctg ggc tat gag tat gtc act Pro Pro Arg Met Asp Ala Lys Met Tyr Leu Gly Tyr Glu Tyr Val Thr 1040 1045 1050	3169
gcc atc cgg aat cta cgg gaa ggc aca tgc cca gaa gcc cca aca gat Ala Ile Arg Asn Leu Arg Glu Gly Thr Cys Pro Glu Ala Pro Thr Asp 1055 1060 1065	3217
gaa tgc aag cct gtg aag tgg tgt gcg ctg agc cac cac gag agg ctc Glu Cys Lys Pro Val Lys Trp Cys Ala Leu Ser His His Glu Arg Leu 1070 1075 1080	3265
aag tgt gat gag tgg agt gtt aac agt gta ggg aaa ata gag tgt gta	3313

Lys Cys Asp Glu Trp	Ser Val Asn Ser Val	Gly Lys Ile Glu Cys Val	
1085	1090	1095	1100
tca gca gag acc acc gaa gac tgc atc gcc aag atc atg aat gga gaa			3361
Ser Ala Glu Thr Thr Glu Asp Cys Ile Ala Lys Ile Met Asn Gly Glu			
	1105	1110	1115
gct gat gcc atg agc ttg gat gga ggg ttt gtc tac ata gcg ggc aag			3409
Ala Asp Ala Met Ser Leu Asp Gly Gly Phe Val Tyr Ile Ala Gly Lys			
	1120	1125	1130
tgt ggt ctg gtg cct gtc ttg gca gaa aac tac aat aag agc gat aat			3457
Cys Gly Leu Val Pro Val Leu Ala Glu Asn Tyr Asn Lys Ser Asp Asn			
	1135	1140	1145
tgt gag gat aca cca gag gca ggg tat ttt gct gta gca gtg gtg aag			3505
Cys Glu Asp Thr Pro Glu Ala Gly Tyr Phe Ala Val Ala Val Val Lys			
	1150	1155	1160
aaa tca gct tct gac ctc acc tgg gac aat ctg aaa ggc aag aag tcc			3553
Lys Ser Ala Ser Asp Leu Thr Trp Asp Asn Leu Lys Gly Lys Lys Ser			
	1165	1170	1175
tgc cat acg gca gtt ggc aga acc gct ggc tgg aac atc ccc atg ggc			3601
Cys His Thr Ala Val Gly Arg Thr Ala Gly Trp Asn Ile Pro Met Gly			
	1185	1190	1195
ctg ctc tac aat aag atc aac cac tgc aga ttt gat gaa ttt ttc agt			3649
Leu Leu Tyr Asn Lys Ile Asn His Cys Arg Phe Asp Glu Phe Phe Ser			
	1200	1205	1210
gaa ggt tgt gcc cct ggg tct aag aaa gac tcc agt ctc tgt aag ctg			3697
Glu Gly Cys Ala Pro Gly Ser Lys Lys Asp Ser Ser Leu Cys Lys Leu			
	1215	1220	1225
tgt atg ggc tca ggc cta aac ctg tgt gaa ccc aac aac aaa gag gga			3745
Cys Met Gly Ser Gly Leu Asn Leu Cys Glu Pro Asn Asn Lys Glu Gly			
	1230	1235	1240
tac tac ggc tac aca ggc gct ttc agg tgt ctg gtt gag aag gga gat			3793
Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Val Glu Lys Gly Asp			
	1245	1250	1255
gtg gcc ttt gtg aaa cac cag act gtc cca cag aac act ggg gga aaa			3841
Val Ala Phe Val Lys His Gln Thr Val Pro Gln Asn Thr Gly Gly Lys			
	1265	1270	1275
aac cct gat cca tgg gct aag aat ctg aat gaa aaa gac tat gag ttg			3889
Asn Pro Asp Pro Trp Ala Lys Asn Leu Asn Glu Lys Asp Tyr Glu Leu			
	1280	1285	1290
ctg tgc ctt gat ggt acc agg aaa cct gtg gag gag tat gcg aac tgc			3937
Leu Cys Leu Asp Gly Thr Arg Lys Pro Val Glu Glu Tyr Ala Asn Cys			
	1295	1300	1305
cac ctg gcc aga gcc ccg aat cac gct gtg gtc aca cgg aaa gat aag			3985
His Leu Ala Arg Ala Pro Asn His Ala Val Val Thr Arg Lys Asp Lys			

1310	1315	1320	
gaa gct tgc gtc cac aag ata tta cgt caa cag cag cac cta ttt gga			4033
Glu Ala Cys Val His Lys Ile Leu Arg Gln Gln Gln His Leu Phe Gly			
1325	1330	1335	1340
agc aac gta act gac tgc tcg ggc aac ttt tgt ttg ttc cgg tcg gaa			4081
Ser Asn Val Thr Asp Cys Ser Gly Asn Phe Cys Leu Phe Arg Ser Glu			
	1345	1350	1355
acc aag gac ctt ctg ttc aga gat gac aca gta tgt ttg gcc aaa ctt			4129
Thr Lys Asp Leu Leu Phe Arg Asp Asp Thr Val Cys Leu Ala Lys Leu			
	1360	1365	1370
cat gac aga aac aca tat gaa aaa tac tta gga gaa gaa tat gtc aag			4177
His Asp Arg Asn Thr Tyr Glu Lys Tyr Leu Gly Glu Glu Tyr Val Lys			
	1375	1380	1385
gct gtt ggt aac ctg aga aaa tgc tcc acc tca tca ctc ctg gaa gcc			4225
Ala Val Gly Asn Leu Arg Lys Cys Ser Thr Ser Ser Leu Leu Glu Ala			
	1390	1395	1400
tgc act ttc cgt aga cct taaaatctca gaggtagggc tgccaccaag			4273
Cys Thr Phe Arg Arg Pro			
1405	1410		
gtgaagatgg gaacgcagat gatccatgag tttgccctgg tttcactggc ccaagtgggt			4333
tgtgctaacc acgtctgtct tcacagctct gtgttgccat gtgtgctgaa caaaaaataa			4393
aaattattat tgattttata tttcgggggg ggggctgcag cccctagacc tgagggtccc			4453
cacctgggac ccttgagagt atcaggtctc ccacgtggga gacaagaaat ccctgtttaa			4513
tatttaaaca gcagtgttcc ccatctgggt ccttgacccc ctcaactctgg cctcagccga			4573
ctgcacagcg gcccctgcat cccctctaga			4603
<210> 4			
<211> 1410			
<212> PRT			
<213> Homo sapiens			
<400> 4			
Met Gly Pro Trp Gly Trp Lys Leu Arg Trp Thr Val Ala Leu Leu Leu			
1	5	10	15
Ala Ala Ala Gly Thr Ala Val Gly Asp Arg Cys Glu Arg Asn Glu Phe			
	20	25	30
Gln Cys Gln Asp Gly Lys Cys Ile Ser Tyr Lys Trp Val Cys Asp Gly			
	35	40	45
Ser Ala Glu Cys Gln Asp Gly Ser Asp Glu Ser Gln Glu Thr Cys Leu			
	50	55	60
Ser Val Thr Cys Lys Ser Gly Asp Phe Ser Cys Gly Gly Arg Val Asn			
	65	70	75
Arg Cys Ile Pro Gln Phe Trp Arg Cys Asp Gly Gln Val Asp Cys Asp			
	85	90	95
Asn Gly Ser Asp Glu Gln Gly Cys Pro Pro Lys Thr Cys Ser Gln Asp			
	100	105	110
Glu Phe Arg Cys His Asp Gly Lys Cys Ile Ser Arg Gln Phe Val Cys			
	115	120	125
Asp Ser Asp Arg Asp Cys Leu Asp Gly Ser Asp Glu Ala Ser Cys Pro			
	130	135	140

Val	Leu	Thr	Cys	Gly	Pro	Ala	Ser	Phe	Gln	Cys	Asn	Ser	Ser	Thr	Cys	145	150	155	160
Ile	Pro	Gln	Leu	Trp	Ala	Cys	Asp	Asn	Asp	Pro	Asp	Cys	Glu	Asp	Gly	165	170		175
Ser	Asp	Glu	Trp	Pro	Gln	Arg	Cys	Arg	Gly	Leu	Tyr	Val	Phe	Gln	Gly	180	185	190	
Asp	Ser	Ser	Pro	Cys	Ser	Ala	Phe	Glu	Phe	His	Cys	Leu	Ser	Gly	Glu	195	200	205	
Cys	Ile	His	Ser	Ser	Trp	Arg	Cys	Asp	Gly	Gly	Pro	Asp	Cys	Lys	Asp	210	215	220	
Lys	Ser	Asp	Glu	Glu	Asn	Cys	Ala	Val	Ala	Thr	Cys	Arg	Pro	Asp	Glu	225	230	235	240
Phe	Gln	Cys	Ser	Asp	Gly	Asn	Cys	Ile	His	Gly	Ser	Arg	Gln	Cys	Asp	245	250		255
Arg	Glu	Tyr	Asp	Cys	Lys	Asp	Met	Ser	Asp	Glu	Val	Gly	Cys	Val	Asn	260	265	270	
Val	Thr	Leu	Cys	Glu	Gly	Pro	Asn	Lys	Phe	Lys	Cys	His	Ser	Gly	Glu	275	280	285	
Cys	Ile	Thr	Leu	Asp	Lys	Val	Cys	Asn	Met	Ala	Arg	Asp	Cys	Arg	Asp	290	295	300	
Trp	Ser	Asp	Glu	Pro	Ile	Lys	Glu	Cys	Gly	Thr	Asn	Glu	Cys	Leu	Asp	305	310	315	320
Asn	Asn	Gly	Gly	Cys	Ser	His	Val	Cys	Asn	Asp	Leu	Lys	Ile	Gly	Tyr	325	330		335
Glu	Cys	Leu	Cys	Pro	Asp	Gly	Phe	Gln	Leu	Val	Ala	Gln	Arg	Arg	Cys	340	345	350	
Glu	Asp	Ile	Asp	Glu	Cys	Gln	Asp	Pro	Asp	Thr	Cys	Ser	Gln	Leu	Cys	355	360	365	
Val	Asn	Leu	Glu	Gly	Gly	Tyr	Lys	Cys	Gln	Cys	Glu	Glu	Gly	Phe	Gln	370	375	380	
Leu	Asp	Pro	His	Thr	Lys	Ala	Cys	Lys	Ala	Val	Gly	Ser	Ile	Ala	Tyr	385	390	395	400
Leu	Phe	Phe	Thr	Asn	Arg	His	Glu	Val	Arg	Lys	Met	Thr	Leu	Asp	Arg	405	410		415
Ser	Glu	Tyr	Thr	Ser	Leu	Ile	Pro	Asn	Leu	Arg	Asn	Val	Val	Ala	Leu	420	425	430	
Asp	Thr	Glu	Val	Ala	Ser	Asn	Arg	Ile	Tyr	Trp	Ser	Asp	Leu	Ser	Gln	435	440	445	
Arg	Met	Ile	Cys	Ser	Thr	Gln	Leu	Asp	Arg	Ala	His	Gly	Val	Ser	Ser	450	455	460	
Tyr	Asp	Thr	Val	Ile	Ser	Arg	Asp	Ile	Gln	Ala	Pro	Asp	Gly	Leu	Ala	465	470	475	480
Val	Asp	Trp	Ile	His	Ser	Asn	Ile	Tyr	Trp	Thr	Asp	Ser	Val	Leu	Gly	485	490		495
Thr	Val	Ser	Val	Ala	Asp	Thr	Lys	Gly	Val	Lys	Arg	Lys	Thr	Leu	Phe	500	505	510	
Arg	Glu	Asn	Gly	Ser	Lys	Pro	Arg	Ala	Ile	Val	Val	Asp	Pro	Val	His	515	520	525	
Gly	Phe	Met	Tyr	Trp	Thr	Asp	Trp	Gly	Thr	Pro	Ala	Lys	Ile	Lys	Lys	530	535	540	
Gly	Gly	Leu	Asn	Gly	Val	Asp	Ile	Tyr	Ser	Leu	Val	Thr	Glu	Asn	Ile	545	550	555	560
Gln	Trp	Pro	Asn	Gly	Ile	Thr	Leu	Asp	Leu	Leu	Ser	Gly	Arg	Leu	Tyr	565	570		575
Trp	Val	Asp	Ser	Lys	Leu	His	Ser	Ile	Ser	Ser	Ile	Asp	Val	Asn	Gly	580	585	590	
Gly	Asn	Arg	Lys	Thr	Ile	Leu	Glu	Asp	Glu	Lys	Arg	Leu	Ala	His	Pro				

595					600					605					
Phe	Ser	Leu	Ala	Val	Phe	Glu	Asp	Lys	Val	Phe	Trp	Thr	Asp	Ile	Ile
610					615					620					
Asn	Glu	Ala	Ile	Phe	Ser	Ala	Asn	Arg	Leu	Thr	Gly	Ser	Asp	Val	Asn
625					630					635					640
Leu	Leu	Ala	Glu	Asn	Leu	Leu	Ser	Pro	Glu	Asp	Met	Val	Leu	Phe	His
				645					650					655	
Asn	Leu	Thr	Gln	Pro	Arg	Gly	Val	Asn	Trp	Cys	Glu	Arg	Thr	Thr	Leu
			660					665					670		
Ser	Asn	Gly	Gly	Cys	Gln	Tyr	Leu	Cys	Leu	Pro	Ala	Pro	Gln	Ile	Asn
		675					680					685			
Pro	His	Ser	Pro	Lys	Phe	Thr	Cys	Ala	Cys	Pro	Asp	Gly	Met	Leu	Leu
690					695					700					
Ala	Arg	Asp	Met	Arg	Ser	Cys	Leu	Thr	Glu	Ala	Glu	Ala	Ala	Val	Ala
705					710					715					720
Thr	Gln	Glu	Thr	Ser	Thr	Val	Arg	Leu	Lys	Val	Val	Pro	Asp	Lys	Thr
				725					730					735	
Val	Arg	Trp	Cys	Ala	Val	Ser	Glu	His	Glu	Ala	Thr	Lys	Cys	Gln	Ser
			740					745					750		
Phe	Arg	Asp	His	Met	Lys	Ser	Val	Ile	Pro	Ser	Asp	Gly	Pro	Ser	Val
		755					760					765			
Ala	Cys	Val	Lys	Lys	Ala	Ser	Tyr	Leu	Asp	Cys	Ile	Arg	Ala	Ile	Ala
770					775					780					
Ala	Asn	Glu	Ala	Asp	Ala	Val	Thr	Leu	Asp	Ala	Gly	Leu	Val	Tyr	Asp
785					790					795					800
Ala	Tyr	Leu	Ala	Pro	Asn	Asn	Leu	Lys	Pro	Val	Val	Ala	Glu	Phe	Tyr
				805					810					815	
Gly	Ser	Lys	Glu	Asp	Pro	Gln	Thr	Phe	Tyr	Tyr	Ala	Val	Ala	Val	Val
			820					825					830		
Lys	Lys	Asp	Ser	Gly	Phe	Gln	Met	Asn	Gln	Leu	Arg	Gly	Lys	Lys	Ser
		835					840					845			
Cys	His	Thr	Gly	Leu	Gly	Arg	Ser	Ala	Gly	Trp	Asn	Ile	Pro	Ile	Gly
850					855					860					
Leu	Leu	Tyr	Cys	Asp	Leu	Pro	Glu	Pro	Arg	Lys	Pro	Leu	Glu	Lys	Ala
865					870					875					880
Val	Ala	Asn	Phe	Phe	Ser	Gly	Ser	Cys	Ala	Pro	Cys	Ala	Asp	Gly	Thr
				885					890					895	
Asp	Phe	Pro	Gln	Leu	Cys	Gln	Leu	Cys	Pro	Gly	Cys	Gly	Cys	Ser	Thr
			900					905					910		
Leu	Asn	Gln	Tyr	Phe	Gly	Tyr	Ser	Gly	Ala	Phe	Lys	Cys	Leu	Lys	Asp
		915					920					925			
Gly	Ala	Gly	Asp	Val	Ala	Phe	Val	Lys	His	Ser	Thr	Ile	Phe	Glu	Asn
		930					935					940			
Leu	Ala	Asn	Lys	Ala	Asp	Arg	Asp	Gln	Tyr	Glu	Leu	Leu	Cys	Leu	Asp
945					950					955					960
Asn	Thr	Arg	Lys	Pro	Val	Asp	Glu	Tyr	Lys	Asp	Cys	His	Leu	Ala	Gln
				965					970					975	
Val	Pro	Ser	His	Thr	Val	Val	Ala	Arg	Ser	Met	Gly	Gly	Lys	Glu	Asp
			980					985					990		
Leu	Ile	Trp	Glu	Leu	Leu	Asn	Gln	Ala	Gln	Glu	His	Phe	Gly	Lys	Asp
		995					1000					1005			
Lys	Ser	Lys	Glu	Phe	Gln	Leu	Phe	Ser	Ser	Pro	His	Gly	Lys	Asp	Leu
		1010					1015					1020			
Leu	Phe	Lys	Asp	Ser	Ala	His	Gly	Phe	Leu	Lys	Val	Pro	Pro	Arg	Met
1025					1030					1035					1040
Asp	Ala	Lys	Met	Tyr	Leu	Gly	Tyr	Glu	Tyr	Val	Thr	Ala	Ile	Arg	Asn
				1045					1050					1055	

Leu Arg Glu Gly Thr Cys Pro Glu Ala Pro Thr Asp Glu Cys Lys Pro
 1060 1065 1070
 Val Lys Trp Cys Ala Leu Ser His His Glu Arg Leu Lys Cys Asp Glu
 1075 1080 1085
 Trp Ser Val Asn Ser Val Gly Lys Ile Glu Cys Val Ser Ala Glu Thr
 1090 1095 1100
 Thr Glu Asp Cys Ile Ala Lys Ile Met Asn Gly Glu Ala Asp Ala Met
 1105 1110 1115 1120
 Ser Leu Asp Gly Gly Phe Val Tyr Ile Ala Gly Lys Cys Gly Leu Val
 1125 1130 1135
 Pro Val Leu Ala Glu Asn Tyr Asn Lys Ser Asp Asn Cys Glu Asp Thr
 1140 1145 1150
 Pro Glu Ala Gly Tyr Phe Ala Val Ala Val Val Lys Lys Ser Ala Ser
 1155 1160 1165
 Asp Leu Thr Trp Asp Asn Leu Lys Gly Lys Lys Ser Cys His Thr Ala
 1170 1175 1180
 Val Gly Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Tyr Asn
 1185 1190 1195 1200
 Lys Ile Asn His Cys Arg Phe Asp Glu Phe Phe Ser Glu Gly Cys Ala
 1205 1210 1215
 Pro Gly Ser Lys Lys Asp Ser Ser Leu Cys Lys Leu Cys Met Gly Ser
 1220 1225 1230
 Gly Leu Asn Leu Cys Glu Pro Asn Asn Lys Glu Gly Tyr Tyr Gly Tyr
 1235 1240 1245
 Thr Gly Ala Phe Arg Cys Leu Val Glu Lys Gly Asp Val Ala Phe Val
 1250 1255 1260
 Lys His Gln Thr Val Pro Gln Asn Thr Gly Gly Lys Asn Pro Asp Pro
 1265 1270 1275 1280
 Trp Ala Lys Asn Leu Asn Glu Lys Asp Tyr Glu Leu Leu Cys Leu Asp
 1285 1290 1295
 Gly Thr Arg Lys Pro Val Glu Glu Tyr Ala Asn Cys His Leu Ala Arg
 1300 1305 1310
 Ala Pro Asn His Ala Val Val Thr Arg Lys Asp Lys Glu Ala Cys Val
 1315 1320 1325
 His Lys Ile Leu Arg Gln Gln Gln His Leu Phe Gly Ser Asn Val Thr
 1330 1335 1340
 Asp Cys Ser Gly Asn Phe Cys Leu Phe Arg Ser Glu Thr Lys Asp Leu
 1345 1350 1355 1360
 Leu Phe Arg Asp Asp Thr Val Cys Leu Ala Lys Leu His Asp Arg Asn
 1365 1370 1375
 Thr Tyr Glu Lys Tyr Leu Gly Glu Glu Tyr Val Lys Ala Val Gly Asn
 1380 1385 1390
 Leu Arg Lys Cys Ser Thr Ser Ser Leu Leu Glu Ala Cys Thr Phe Arg
 1395 1400 1405
 Arg Pro
 1410

<210> 5

<211> 24

<212> DNA

<213> Homo sapiens

<400> 5

gctgtggcca cctgtcgccc tgac

<210> 6

<211> 60

<212> DNA
 <213> Homo sapiens

<400> 6
 tgcacacccat ctcacagttt tatcagggac cacagccttg caggccttcg tgtgggggtc 60

<210> 7
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 7
 gcctcgaagc tggttcatct g 21

<210> 8
 <211> 59
 <212> DNA
 <213> Homo sapiens

<400> 8
 gacccccaca cgaaggcctg caaggctgtg gtccctgataa aactgtgaga tgggtgtgca 59

<210> 9
 <211> 48
 <212> DNA
 <213> Homo sapiens

<400> 9
 tgcacacccat ctcacagttt tatcagggac gaccttttagc ctgacggt 48

<210> 10
 <211> 19
 <212> DNA
 <213> Homo sapiens

<400> 10
 tcagtggccc aatggcatc 19

<210> 11
 <211> 51
 <212> DNA
 <213> Homo sapiens

<400> 11
 caggagacat ccaccgtcag gctaaaggtc gtccctgata aaactgtgag a 51

<210> 12
 <211> 18
 <212> DNA
 <213> Homo sapiens

<400> 12
 cttcccatga ggagagct 18

B
 concl